



PCT

## RAW SEQUENCE LISTING

DATE: 01/05/2004

PATENT APPLICATION: US/10/070,794A

TIME: 11:33:39

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\01052004\J070794A.raw

4 <110> APPLICANT: ANDERSSON, Leif  
 5 LOOFT, Christian  
 6 KALM, Ernst  
 7 MILAN, Denis  
 8 ROBIC, Annie  
 9 ROGEL-GAILLARD, Claire  
 10 IANNUCELLI, Nathalie  
 11 GELLIN, Joel  
 12 LE ROY, Pascale  
 13 CHARDON, Patrick  
 15 <120> TITLE OF INVENTION: VARIANTS OF THE GAMMA CHAIN OF AMPK, DNA SEQUENCES ENCODING  
 16 THE SAME, AND USES THEREOF  
 18 <130> FILE REFERENCE: 11145-023US1  
 20 <140> CURRENT APPLICATION NUMBER: US 10/070,794A  
 C--> 21 <141> CURRENT FILING DATE: 2003-05-23  
 23 <150> PRIOR APPLICATION NUMBER: PCT/EP00/09896  
 24 <151> PRIOR FILING DATE: 2000-09-11  
 26 <150> PRIOR APPLICATION NUMBER: EP 00401388.4  
 27 <151> PRIOR FILING DATE: 2000-05-18  
 29 <150> PRIOR APPLICATION NUMBER: EP 99402236.3  
 30 <151> PRIOR FILING DATE: 1999-09-10  
 32 <160> NUMBER OF SEQ ID NOS: 42

Does Not Comply  
 Corrected Diskette Needed  
 (pg. 3,5)

## ERRORED SEQUENCES

622 <210> SEQ ID NO: 27  
 623 <211> LENGTH: 1873  
 624 <212> TYPE: DNA  
 625 <213> ORGANISM: Sus scrofa  
 627 <220> FEATURE:  
 628 <221> NAME/KEY: CDS  
 629 <222> LOCATION: (1)..(1395)  
 631 <400> SEQUENCE: 27  
 632 atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct 48  
 633 Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala  
 634 1 5 10 15  
 636 gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96  
 637 Val Thr Thr Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
 638 20 25 30  
 640 tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144  
 641 Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly  
 642 35 40 45

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644 ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192
645 Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
646      50                      55                      60
648 gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240
649 Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
650 65                      70                      75                      80
652 gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac 288
653 Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
654      85                      90                      95
656 tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc 336
657 Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
658      100                     105                     110
660 ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg 384
661 Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
662      115                     120                     125
664 gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg 432
665 Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
666      130                     135                     140
668 ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg 480
669 Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
670 145                     150                     155                     160
672 cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc 528
673 His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
674      165                     170                     175
676 aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt 576
677 Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
678      180                     185                     190
680 gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag 624
681 Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
682      195                     200                     205
684 aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg 672
685 Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
686      210                     215                     220
688 ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa 720
689 Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
690 225                     230                     235                     240
692 gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc 768
693 Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
694      245                     250                     255
696 aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc 816
697 Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
698      260                     265                     270
700 tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct 864
701 Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
702      275                     280                     285
704 gtc tcc ggg gct gtg,ctc cac atc ctc aca cat aag cgg ctt ctc aag 912
705 Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
706      290                     295                     300
708 ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac 960

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709 Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
710 305          310          315          320
712 cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg 1008
713 Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
714          325          330          335
716 gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac 1056
717 Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
718          340          345          350
720 cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg 1104
721 Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
722          355          360          365
724 ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca 1152
725 Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
726          370          375          380
728 tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca 1200
729 Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
730 385          390          395          400
732 ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg 1248
733 Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
734          405          410          415
737 gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc 1296
738 Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
739          420          425          430
742 gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc 1344
743 Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
744          435          440          445
746 ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc 1392
747 Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
748          450          455          460
750 tga gaaccttgga acctttgctc tcaggccacc tggcacacct ggaagccagt 1445
E--> 752 465 delete
754 gaaggagacc gtggactcag ctctcacttc ccctcagccc cacttgctgg tctggtcttt 1505
756 gttcaggtag gctccgcccg gggcccctgg cctcagcatc agcccctcag tctccctggg 1565
758 caccagatc tcagactggg gcaccctgaa gatgggagtg gccagctta tagctgagca 1625
760 gccttgtgaa atctaccagc atcaagactc actgtgggac cactgctttg tccattctc 1685
762 agctgaaatg atggagggcc tcataagagg ggtggacagg gcctggagta gaggccagat 1745
764 cagtgacgtg ccttcaggac ctccggggag ttagagctgc cctctctcag ttcagttccc 1805
766 ccctgctgag aatgtccctg gaaggaagcc agttaataaa ccttggttgg atggaatttg 1865
768 gagagtcg 1873
837 <210> SEQ ID NO: 29
838 <211> LENGTH: 2115
839 <212> TYPE: DNA
840 <213> ORGANISM: Homo sapiens
842 <220> FEATURE:
843 <221> NAME/KEY: CDS
844 <222> LOCATION: (1)..(1395)
846 <400> SEQUENCE: 29
847 atg agc ttc cta gag caa gaa aac agc agc tca tgg cca tca cca gct 48
848 Met Ser Phe Leu Glu Gln Glu Asn Ser Ser Ser Trp Pro Ser Pro Ala

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849	1	5	10	15	
851	gtg acc agc agc tca gaa aga atc cgt ggg aaa cgg agg gcc aaa gcc	96			
852	Val Thr Ser Ser Ser Glu Arg Ile Arg Gly Lys Arg Arg Ala Lys Ala				
853	20 25 30				
856	ttg aga tgg aca agg cag aag tgc gtg gag gaa ggg gag cca cca ggt	144			
857	Leu Arg Trp Thr Arg Gln Lys Ser Val Glu Glu Gly Glu Pro Pro Gly				
858	35 40 45				
860	cag ggg gaa ggt ccc cgg tcc agg cca act gct gag tcc acc ggg ctg	192			
861	Gln Gly Glu Gly Pro Arg Ser Arg Pro Thr Ala Glu Ser Thr Gly Leu				
862	50 55 60				
864	gag gcc aca ttc ccc aag acc aca ccc ttg gct caa gct gat cct gcc	240			
865	Glu Ala Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala				
866	65 70 75 80				
868	ggg gtg ggc act cca cca aca ggg tgg gac tgc ctc ccc tct gac tgt	288			
869	Gly Val Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys				
870	85 90 95				
872	aca gcc tca gct gca ggc tcc agc aca gat gat gtg gag ctg gcc acg	336			
873	Thr Ala Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr				
874	100 105 110				
876	gag ttc cca gcc aca gag gcc tgg gag tgt gag cta gaa ggc ctg ctg	384			
877	Glu Phe Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Glu Gly Leu Leu				
878	115 120 125				
880	gaa gag agg cct gcc ctg tgc ctg tcc ccg cag gcc cca ttt ccc aag	432			
881	Glu Glu Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys				
882	130 135 140				
884	ctg ggc tgg gat gac gaa ctg cgg aaa ccc ggc gcc cag atc tac atg	480			
885	Leu Gly Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met				
886	145 150 155 160				
888	cgc ttc atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc	528			
889	Arg Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser				
890	165 170 175				
892	aag cta gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt	576			
893	Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe				
894	180 185 190				
896	gct ctg gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag	624			
897	Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys				
898	195 200 205				
900	aag cag agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg	672			
901	Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val				
902	210 215 220				
904	ctg cat cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa	720			
905	Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu				
906	225 230 235 240				
908	caa cat aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc	768			
909	Gln His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe				
910	245 250 255				
913	aag cct ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc	816			
914	Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val				
915	260 265 270				

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```

917 tac acc ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg      864
918 Tyr Thr Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
919      275      280      285
921 gtg tca ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag      912
922 Val Ser Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
923      290      295      300
925 ttc ctg cac atc ttt ggt tcc ctg ctg ccc cgg ccc tcc ttc ctc tac      960
926 Phe Leu His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr
927 305      310      315      320
929 cgc act atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg      1008
930 Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
931      325      330      335
933 gtg ctg gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac      1056
934 Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
935      340      345      350
937 cgg cgt gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg      1104
938 Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val
939      355      360      365
941 ggc ctc tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc      1152
942 Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
943      370      375      380
945 tac aac cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca      1200
946 Tyr Asn His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr
947 385      390      395      400
949 cta tgt ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg      1248
950 Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly
951      405      410      415
953 gaa gtg atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta      1296
954 Glu Val Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu
955      420      425      430
957 gtg gac gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc      1344
958 Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
959      435      440      445
961 ctt cag gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc      1392
962 Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
963      450      455      460
965 tga gaagatctga gtctctcaatc ccaagccaac tgcacactgg aagccaatga      1445
E--> 967 465
970 aggaattgag aacagcttca tttccccaac cccaatttgc tggttcagct atgattcagg 1505
972 cttcttcagc cttccaaaat tgcctttgcc ttactttgtc tcccagaacc cttcgggcat 1565
974 gccagtgca ccatgggatg atgaaattaa ggagaacagc tgagtcaagc ttggagggtcc 1625
976 ctgaaccaga ggcactagga ttaccccagg gccatctgtg ctccatgccc gcccatcccc 1685
978 ttgccgcctg actgggtcgg atggcccagg tgggtttagt cagggcttct ggattcctcg 1745
980 gtttctgggc tacctatggc ttacgccttc agtccctggg agtcccagct gttgttccca 1805
982 gcaacgtcgc cactgccctc ctactctcca ggctttgtca tttcaaggct gctgaaatgc 1865
984 tgcatttcag gggccaccat ggcagagccg ttatttatag aactgcctgt tggaggtggg 1925
986 gagtctccc tccattcttg tccagaaaac tccttagctc tcgcagtgag ccatgttctt 1985
988 agtctccagg gatggatggc cttgtatatg gacccttgag aatgagcaat tgagaaaaca 2045
990 aaacaaaagg aacaatccat gaacttagat tttattgggt tcaactcaaaa tgctgcagtc 2105

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Input Set : A:\PTO.FG.txt

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992 atttgacctg

2115

VERIFICATION SUMMARY

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Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\01052004\J070794A.raw

L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:752 M:254 E: No. of Bases conflict, this line has no nucleotides.

L:967 M:254 E: No. of Bases conflict, this line has no nucleotides.